Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (currently amended) A method for diagnosing prostate cancer versus benign prostate hyperplasia, the method comprising:

i. obtaining from a subject a sample containing a plurality of prostrate related protein markers having apparent molecular weights below 10,000 Da wherein the sample is selected from the group consisting of prostate tissue, blood, serum, semen, seminal fluid or seminal plasma;

ii. determining by mass spectroscopy a representative pattern [test amount] of the quantity of a plurality of protein markers in the sample, the protein markers having an apparent molecular weight of less than 10,000 Da;

iii. comparing the pattern [test amount] of the plurality of protein markers having apparent molecular weight of less than 10,000 Da with an amount of a plurality of protein markers having an apparent molecular weight of less than 10,000 Da from a control sample where the control sample originates from benign prostate hyperplasia;
and

iv. determining whether the [test amount] pattern of the sample is a diagnostic amount consistent with a diagnosis of prostate cancer versus benign prostate hyperplasia where the pattern consistent with a diagnosis of prostate cancer [diagnostic amount] is represented by an increase in the quantity of lower molecular weight proteins.

Claims 2-7 (canceled)

8. (previously presented) The method of claim 1, wherein the seminal fluid sample is selected from the group consisting of semen and seminal plasma.

Claims 9-11 (canceled)

12. (previously presented) The method of claim 1, the method further comprising:

(a) generating data on the sample with the mass spectrometer indicating intensity of signal for mass/charge ratios;

(b) transforming the data into computer-readable form; and

(c) operating a computer to execute an algorithm, wherein the algorithm determines closeness-of-fit between the computer-readable data and data indicating a diagnosis of prostate cancer or a negative diagnosis.

Claims 13-19 (canceled)

20. (previously presented) The method of claim 1, wherein the sample is seminal plasma.

Claims 21-83 (canceled)

84. (previously presented) The method of claim 1 where the protein markers are adsorbed onto a probe comprising an adsorbent of a hydrophilic polymer.

85. (previously presented) The method of claim 1 where the protein markers are adsorbed onto a probe comprising a metal binding group.

86. (previously presented) The method of claim 84 where the adsorbent comprises a hydrophobic group.

87. (previously presented) The method of claim 84 where the adsorbent comprises a cationic group.

88. (previously presented) The method of claim 84 where the adsorbent comprises a metal ion chelating group.

89. (previously presented) The method of claim 20, the method further comprising:

(a) generating data on the sample with the mass spectrometer indicating intensity of signal for mass/charge ratios;

(b) transforming the data into computer-readable form; and

(c) operating a computer to execute an algorithm, wherein the algorithm determines closeness-of-fit between the computer-readable data and data indicating a diagnosis of prostate cancer or a negative diagnosis.

90. (previously presented) The method of claim 20 where the protein markers are adsorbed onto a probe comprising an adsorbent of a hydrophilic polymer.

91. (previously presented) The method of claim 20 where the protein markers are adsorbed onto a probe comprising a metal binding group.

92. (previously presented) The method of claim 90 where the adsorbent comprises a hydrophobic group.

93. (previously presented) The method of claim 90 where the adsorbent comprises a cationic group.

94. (previously presented) The method of claim 90 where the adsorbent comprises a metal ion chelating group.